

Query= SEQ ID NO:1
(2772 letters)

Score E
(bits) Value

Sequences producing significant alignments:

AL365232.24.1.120846	<u>1913</u>	0.0
AL445569.1.1.47057	<u>733</u>	0.0
AL360236.26.1.154998	<u>355</u>	1e-94

>AL365232.24.1.120846
Length = 120846

Score = 1913 bits (965), Expect = 0.0

Identities = 965/965 (100%)

Strand = Plus / Plus

Query: 1808 aggtacagtccatagaatccaagctggactgcctactagacatctatcaacaggccttc 1867
|||||||
Sbjct: 61339 aggtacagtccatagaatccaagctggactgcctactagacatctatcaacaggccttc 61398

Query: 1868 ggaaaggctctgcctcagccctcgcttggcttcatccagatcccacctttgaatgtg 1927
|||||||
Sbjct: 61399 ggaaaggctctgcctcagccctcgcttggcttcatccagatcccacctttgaatgtg 61458

Query: 1928 aacagacatctgactatcaaagccctgtggatagcaaagatcttcgggttccgcacaaa 1987
|||||||
Sbjct: 61459 aacagacatctgactatcaaagccctgtggatagcaaagatcttcgggttccgcacaaa 61518

Query: 1988 acagtggctgcttatccagatcaacttagtgccaaacatctcgagaggcctgcagttcattc 2047
|||||||
Sbjct: 61519 acagtggctgcttatccagatcaacttagtgccaaacatctcgagaggcctgcagttcattc 61578

Query: 2048 tgacccaaatgagttcagtgccagactttctacgcgcttagccctactatgcacagtc 2107
|||||||
Sbjct: 61579 tgacccaaatgagttcagtgccagactttctacgcgcttagccctactatgcacagtc 61638

Query: 2108 aagcaacacaggtgccaattagtcaaagcgatggctcagcagtggcagccaccaacacca 2167
|||||||
Sbjct: 61639 aagcaacacaggtgccaattagtcaaagcgatggctcagcagtggcagccaccaacacca 61698

Query: 2168 ttgcaaaccataatacggcaccaagccagcagccccacaactttacagatccac 2227
|||||||
Sbjct: 61699 ttgcaaaccataatacggcaccaagccagcagccccacaactttacagatccac 61758

Query: 2228 ctcctctcccagccatcaagcatctgccaggccagaaactctgcaccttaaccctgcag 2287
|||||||
Sbjct: 61759 ctcctctcccagccatcaagcatctgccaggccagaaactctgcaccttaaccctgcag 61818

Query: 2288 gcttacaggaaagcatttctgacgtcaccacctgccttgcctccaaggaaaatgttc 2347
|||||||
Sbjct: 61819 gcttacaggaaagcatttctgacgtcaccacctgccttgcctccaaggaaaatgttc 61878

Query: 2348 aggttgcacagtcaaattctcaccaaggaccgttatgagggaaaagcttgacatggag 2407
|||||||
Sbjct: 61879 aggttgcacagtcaaattctcaccaaggaccgttatgagggaaaagcttgacatggag 61938

Query: 2408 gagaaactctgttgtctgtccatgggccgaaggacttggcaaatcttgc 2467
|||||||
Sbjct: 61939 gagaaactctgttgtctgtccatgggccgaaggacttggcaaatcttgc 61998

Query: 2468 tgcaaaacctgatcaggtcgaccgaggaactgaatacataactttcaggagtgactcaa 2527
|||||||
Sbjct: 61999 tgcaaaacctgatcaggtcgaccgaggaactgaatacataactttcaggagtgactcaa 62058

Query: 2528 gtggctccagaggcagccaaagatttacccaaatggagggaatccaaattgttataa 2587
|||||||
Sbjct: 62059 gtggctccagaggcagccaaagatttacccaaatggagggaatccaaattgttataa 62118

Query: 2588 ctgatgaagaggtggtcccgaagagagacagacactttgatgccgcaccgcagc 2647
|||||||
Sbjct: 62119 ctgatgaagaggtggtcccgaagagagacagacactttgatgccgcaccgcagc 62178

Query: 2648 ctgccaggaaagctgccttgcatacgactctctaaggacttgcacgatcatctc 2707
|||||||
Sbjct: 62179 ctgccaggaaagctgccttgcatacgactctctaaggacttgcacgatcatctc 62238

Query: 2708 agagcattttaaggcaggagaaagtacagatgcctcagttgcctcatgtcaaactga 2767
|||||||
Sbjct: 62239 agagcattttaaggcaggagaaagtacagatgcctcagttgcctcatgtcaaactga 62298

Query: 2768 aataa 2772
|||||
Sbjct: 62299 aataa 62303

Score = 438 bits (221), Expect = e-120
Identities = 221/221 (100%)
Strand = Plus / Plus

Query: 1221 tcagaagctaagtttaaggagcgagtgcgcattggctagccccagggccagagtattaa 1280
|||||||
Sbjct: 310 tcagaagctaagtttaaggagcgagtgcgcattggctagccccagggccagagtattaa 369

Query: 1281 gagccgacaagcctcagttaggtacaggaggtccccaaagcaccgacatcacagccgaggg 1340
Sbjct: 370 gagccgacaagcctcagttaggtacaggaggtccccaaagcaccgacatcacagccgaggg 429

Query: 1341 cagtcccaccaaagtgcagaagagctggagcttcaacgaccgaacccgcttcggccctc 1400
Sbjct: 430 cagtcccaccaaagtgcagaagagctggagcttcaacgaccgaacccgcttcggccctc 489

Query: 1401 gctgcgcctcaaaagttctcagccaaaaccagtgatagatg 1441
Sbjct: 490 gctgcgcctcaaaagttctcagccaaaaccagtgatagatg 530

Score = 268 bits (135), Expect = 2e-68
Identities = 135/135 (100%)
Strand = Plus / Plus

Query: 1548 cagaatttatgaaatttcatgttgcacaaacggaagtttaaggaaacattacgtccatatga 1607
Sbjct: 57459 cagaatttatgaaatttcatgttgcacaaacggaagtttaaggaaacattacgtccatatga 57518

Query: 1608 tgtaaaagatgtcattgaacaatattctgctggcatctggacatgttgtttagaattaa 1667
Sbjct: 57519 tgtaaaagatgtcattgaacaatattctgctggcatctggacatgttgtttagaattaa 57578

Query: 1668 aagccttcaaacacg 1682
Sbjct: 57579 aagccttcaaacacg 57593

Score = 264 bits (133), Expect = 3e-67
Identities = 133/133 (100%)
Strand = Plus / Plus

Query: 1682 gtgttgcataattttggaaaaggccaaatcacatcagataagaagagccgagaaaaaa 1741
Sbjct: 59453 gtgttgcataattttggaaaaggccaaatcacatcagataagaagagccgagaaaaaa 59512

Query: 1742 taacagcagaacatgagaccacagacgatctcagttatgctcggtcggtggcaaggttg 1801
Sbjct: 59513 taacagcagaacatgagaccacagacgatctcagttatgctcggtcggtggcaaggttg 59572

Query: 1802 aaaaacaggtaca 1814
Sbjct: 59573 aaaaacaggtaca 59585

Score = 218 bits (110), Expect = 1e-53
Identities = 110/110 (100%)
Strand = Plus / Plus

Query: 1441 gctgacacagcccttggcactgtatgtatgtaaaaaggatgccagtgtatgtta 1500
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 36634 gctgacacagcccttggcactgtatgtatgtaaaaaggatgccagtgtatgtta 36693

Query: 1501 tcagtggaaagacctccccccaccacttaaaaactgtcattcgagctatcatg 1550
Sbjct: 36694 tcagtggaaagacctccccccaccacttaaaaactgtcattcgagctatcatg 36743

>AL445569.1.1.47057
Length = 47057

Score = 733 bits (370), Expect = 0.0
Identities = 394/401 (98%), Gaps = 6/401 (1%)
Strand = Plus / Plus

Query: 1 atgccccggcaccacgcggaggagaggagggcgccgcgggtctgggtgaagagc 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 4316 atgccccggcaccacgcggaggagaggagggcgccgcgggtctgggtgaagagc 4375

Query: 61 ggcgca...gtggatgtggag 120
Sbjct: 4376 ggcc...gtggatgtggag 4435

Query: 121 tcgggccggggcagggtgctgctgaactcgccagccggccaggggcgacggcctgtactg 180
||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 4436 tccggccggggcagggtgctgctgaactcgccagccggccaggggcgacggcctgtactg 4495

Query: 181 ctgggcacccgcgccggcacgctcggtggcggcggcggctgagggagagccggccgg 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 4496 ctgggcacccacacacggccacqctcqatqqcqgqccqgqgtggcctgagggagagccggccgg 4555

Query: 241 ggcaaggcagggggcccgatgagcctgctgggaagccgcgtctttacacgacttagccag 300
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 4556 ggcaaggcagggggcccgatgagcctgctgggaagccgcgtctttacacgacttagccag 4615

Query: 361 agaccccgccggctggcggtcatctaccacgcttcgt 398
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sblast: 4676 agaccccgccggctggcggtcatctaccacgcttcgt 4713

>AL360236.26.1.154998
Length = 154998

Score = 355 bits (179), Expect = 1e-94
Identities = 179/179 (100%)
Strand = Plus / Plus

```
Query: 615 agataccattgttcttatcgctcaatagcagttgttctgcaaaaactcaggtaatat 674
          ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 99107 agataccattgttcttatcgctcaatagcagttgttctgcaaaaactcaggtaatat 99166
```

Query: 675 ttttgcacgtctgactcagaagtctccgttccatacagatcctccgatggcgcat 734
Sbjct: 99167 ttttgcacgtctgactcagaagtctccgttccatacagatcctccgatggcgcat 99226

Query: 735 ggaccgaaggggaggcacttggaaattactgggttcagtggttatgctcacagcaagg 793
Sbjct: 99227 qqaccgaaggggaggcacttggaaattactgggttcagtggttatgctcacagcaagg 99285

Score = 254 bits (128), Expect = 3e-64
Identities = 128/128 (100%)
Strand = Plus / Plus

Query: 489 ggagttcggtatgatttcgtcttgggttggagttcatcattcaatctggctgcggg 548
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 63722 ggagttcggtatgatttcgtcttgggttggagttcatcattcaatctggctgcggg 63781

Query: 549 ttgctgttgcataatagaggatggcaaggaaactgaggttgctcgaaagccttctg 608
Sbjct: 63782 ttgctgttgcataatagaggatggcaaggaaactgaggttgctcgaaagccttctg 63841

Query: 609 tgttata 616
|||
Sbjct: 63842 tgttata 63849

Score = 254 bits (128), Expect = 3e-64
Identities = 128/128 (100%)
Strand = Plus / Plus

Query: 791 aggaattaatcacagcttggtacataggattttgggttcttatttttcgtcttccttg 850
Sbjct: 99547 aggaattaatcacagcttggtacataggattttgggttcttatttttcgtcttccttg 99606

Query: 851 tctatctggtgaaaaggatgccaataaaagagtttctacatatgcagatgctctgg 910
|||||||
Sbjct: 99607 tctatctggtgaaaaggatgccaataaaagagtttctacatatgcagatgctctgg 99666

Query: 911 ggggcaca 918
|||||||
Sbjct: 99667 ggggcaca 99674

Score = 222 bits (112), Expect = 9e-55
Identities = 112/112 (100%)
Strand = Plus / Plus

Query: 919 attacattgacaactattggctatggagacaaaactccctaacttgctggaaagattg 978
|||||||
Sbjct: 127044 attacattgacaactattggctatggagacaaaactccctaacttgctggaaagattg 127103

Query: 979 ctttctgcaggcttgcactccttgcatttcatttgcacttcctgccg 1030
|||||||
Sbjct: 127104 ctttctgcaggcttgcactccttgcatttcatttgcacttcctgccg 127155

Score = 194 bits (98), Expect = 2e-46
Identities = 98/98 (100%)
Strand = Plus / Plus

Query: 1123 cagtgtgttggcgtagttacgcagctgatgagaaatctgtttcattgcaacctggaaag 1182
|||||||
Sbjct: 142267 cagtgtgttggcgtagttacgcagctgatgagaaatctgtttcattgcaacctggaaag 142326

Query: 1183 ccacacttgaaggccttgcacacctgcagccctaccaa 1220
|||||||
Sbjct: 142327 ccacacttgaaggccttgcacacctgcagccctaccaa 142364

Score = 190 bits (96), Expect = 3e-45
Identities = 96/96 (100%)
Strand = Plus / Plus

Query: 1030 ggcattctggctcaggtttgcattaaaagtacaagaacaacaccgccagaaacacttt 1089
|||||||
Sbjct: 133095 ggcattctggctcaggtttgcattaaaagtacaagaacaacaccgccagaaacacttt 133154

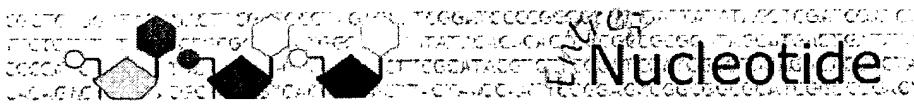
Query: 1090 gagaaaagaaggaacccagctgccaacctcattcag 1125
|||||||
Sbjct: 133155 gagaaaagaaggaacccagctgccaacctcattcag 133190

Score = 182 bits (92), Expect = 8e-43
Identities = 92/92 (100%)
Strand = Plus / Plus

Query: 399 ttttctccgtcttggtgcggatggatgtcagttttctaccatccctgagcacac 458
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 25695 ttttctccgtcttggtgcggatggatgtcagttttctaccatccctgagcacac 25754

Query: 459 aaaattggcctcaagggtgcctttatcctgg 490
||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 25755 aaaattggcctcaagggtgcctttatcctgg 25786

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Display default Show: 20 File Features

1: AL365232. Human DNA sequenc...[gi:13234949]

Links

LOCUS AL365232 120846 bp DNA linear PRI 01-MAR-2001

DEFINITION Human DNA sequence from clone RP11-257K9 on chromosome 6, complete sequence.

ACCESSION AL365232

VERSION AL365232.24 GI:13234949

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 120846)

AUTHORS Williams,S.

TITLE Direct Submission

JOURNAL Submitted (01-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT On Mar 5, 2001 this sequence version replaced gi:13160293. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6> RP11-257K9 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-257K9 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP11-257K9 is at 1 in this sequence. The

NCBI




Search **Nucleotide** for **Go** **Clear**

Limits	Preview/Index	History	Clipboard	Details
Display <input type="button" value="default"/>	Show: <input type="button" value="20"/>	Send to <input type="button" value="File"/>	Get Subsequence	Features

[1: AL445569. Human DNA sequenc...[gi:10862812]

Links

LOCUS AL445569 47057 bp DNA linear PRI 17-OCT-2000
DEFINITION Human DNA sequence from clone RP11-135M8 on chromosome 6, complete sequence.
ACCESSION AL445569 AL161434
VERSION AL445569.1 GI:10862812
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 47057)
AUTHORS Bates,K.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>
RP11-135M8 is from the library RPCI-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/>
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-135M8 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true right end of clone RP3-474G15 is at 100 in this sequence.
The true right end of clone RP11-135M8 is at 47057 in this sequence.



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Features

[1: AL360236. Human DNA sequenc...[gi:13398790]]

Links

LOCUS AL360236 154998 bp DNA linear PRI 19-MAR-2001
DEFINITION Human DNA sequence from clone RP11-380M3 on chromosome 6, complete sequence.
ACCESSION AL360236
VERSION AL360236.26 GI:13398790
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 154998)
AUTHORS Clark,G.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT On Mar 21, 2001 this sequence version replaced gi:13161652. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6> RP11-380M3 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-380M3 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-380M3 is at 1 in this sequence. The